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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/923,444

DATE: 10/16/2001
TIME: 15:02:12

Input Set : N:\Crf3\RULE60\09923444.txt
Output Set: N:\CRF3\10162001\I923444.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: LI, YI
 7 FLEISCHMANN, ROBERT
 9 (ii) TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER
 11 (iii) NUMBER OF SEQUENCES: 6
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Human Genome Sciences, Inc.
 15 (B) STREET: 9410 Key West Avenue
 16 (C) CITY: Rockville
 17 (D) STATE: MD
 18 (E) COUNTRY: US
 19 (F) ZIP: 20850
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/923,444
 C--> 29 (B) FILING DATE: 08-Aug-2001
 30 (C) CLASSIFICATION:
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: 09/062,815
 34 (B) FILING DATE: 199-12-20
 36 (viii) ATTORNEY/AGENT INFORMATION:
 37 (A) NAME: Michele M. Wales
 38 (B) REGISTRATION NUMBER: 43,975
 39 (C) REFERENCE/DOCKET NUMBER: PF116
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: (301) 309-8504
 43 (B) TELEFAX: (301) 309-8439
 46 (2) INFORMATION FOR SEQ ID NO: 1:
 48 (i) SEQUENCE CHARACTERISTICS:
 49 (A) LENGTH: 2485 base pairs
 50 (B) TYPE: nucleic acid
 51 (C) STRANDEDNESS: single
 52 (D) TOPOLOGY: linear
 54 (ii) MOLECULE TYPE: DNA (genomic)
 57 (ix) FEATURE:
 58 (A) NAME/KEY: CDS
 59 (B) LOCATION: 266..2446
 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 64 CGGAGGCAGG GAGTGAGGAG CGAGCGGAGT CGCGTGCAGCC GGCGCGAGCT CCGGGTCGCC 60
 66 CCAGCCCCAG CGGGGGGCCT GTGGCGGGGG AGGAGCTGTG CGTCCGCGAC CCGTCGGGAT 120
 68 CGCAGCTGCT CGGCCGGAGT GCACGGGCCG AGTCTGCGCG ACTACCCACG CGTGACAGGT 180
 70 CCCTGAATGA GAAGGAGCTG ACAGCAGCTG AATTCCATCT TCTCTGTGTG CTGGGGAGCA 240

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72	GGGCTACACG	GCCCAGGTGG	CATCA	ATG CCG AAG AAC AGC AAA GTG ACC CAG	292
73				Met Pro Lys Asn Ser Lys Val Thr Gln	
74			1	5	
76	CGT GAG CAC AGC AGT GAG	CAT GTC ACT GAG	TCC GTG	GCC GAC CTG CTG	340
77	Arg Glu His Ser Ser	Glu His Val Thr	Glu Ser Val Ala	Asp Leu Leu	
78	10	15	20	25	
80	GCC CTC GAG GAG CCT GTG GAC TAT AAG CAG AGT	GTA CTG AAT GTG GCT	388		
81	Ala Leu Glu Glu Pro Val Asp Tyr Lys Gln Ser Val Leu Asn Val Ala				
82	30	35	40		
84	GGT GAG GCA GGC GGC AAG CAG AAG GCG GTG GAG GAG	CTG GAT GCA	436		
85	Gly Glu Ala Gly Gly Lys Gln Lys Ala Val Glu Glu Leu Asp Ala				
86	45	50	55		
88	GAG GAC CCG CCG GCC TGG AAC AGT AAG CTG CAG TAC ATC	CTG GCC CAG	484		
89	Glu Asp Arg Pro Ala Trp Asn Ser Lys Leu Gln Tyr Ile Leu Ala Gln				
90	60	65	70		
92	ATT GGC TTC TCT GTG GGC CTC GGC AAC ATC TGG AGG TTC CCC TAC CTG	532			
93	Ile Gly Phe Ser Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr Leu				
94	75	80	85		
96	TGC CAG AAA AAT GGA GGA GGT GCT TAC CTG GTG CCC TAC CTG GTG CTG	580			
97	Cys Gln Lys Asn Gly Gly Ala Tyr Leu Val Pro Tyr Leu Val Leu				
98	90	95	100	105	
100	CTG ATC ATC ATC GGG ATC CCC CTC TTC CTG GAG CTG GCT GTG GGT	628			
101	Leu Ile Ile Ile Gly Ile Pro Leu Phe Phe Leu Glu Leu Ala Val Gly				
102	110	115	120		
104	CAG AGG ATC CGC CGC GGA AGC ATC GGT GTG TGG CAC TAT ATA TGT CCC	676			
105	Gln Arg Ile Arg Arg Gly Ser Ile Gly Val Trp His Tyr Ile Cys Pro				
106	125	130	135		
108	CGC CTG GGG GGG ATC GGC TTC TCC AGC TGC ATA GTC TGT CTC TTT GTG	724			
109	Arg Leu Gly Gly Ile Gly Phe Ser Ser Cys Ile Val Cys Leu Phe Val				
110	140	145	150		
112	GGG CTG TAT TAT AAT GTG ATC ATC GGG TGG AGC ATC TTC TAT TTC TTC	772			
113	Gly Leu Tyr Tyr Asn Val Ile Ile Gly Trp Ser Ile Phe Tyr Phe Phe				
114	155	160	165		
116	AAG TCC TTC CAG TAC CCG CTG CCC TGG AGT GAA TGT CCT GTC GTC AGG	820			
117	Lys Ser Phe Gln Tyr Pro Leu Pro Trp Ser Glu Cys Pro Val Val Arg				
118	170	175	180	185	
120	AAT GGG AGC GTC GCA GTG GTG GAG GCA GAG TGT GAA AAG AGC TCA GCC	868			
121	Asn Gly Ser Val Ala Val Val Glu Ala Glu Cys Glu Lys Ser Ser Ala				
122	190	195	200		
124	ACT ACC TAC TTC TGG TAC CGA GAG GCT TTG GAC ATC TCT GAC TCC ATC	916			
125	Thr Thr Tyr Phe Trp Tyr Arg Glu Ala Leu Asp Ile Ser Asp Ser Ile				
126	205	210	215		
128	TCG GAG AGT GGG GGC CTC AAC TGG AAG ATG ACC CTG TGC CTC CTC GTG	964			
129	Ser Glu Ser Gly Gly Leu Asn Trp Lys Met Thr Leu Cys Leu Leu Val				
130	220	225	230		
132	GTC TGG AGC ATC GGG GGG ATG GCT GTC GGT AAG GGC ATC CAG TCC TCG	1012			
133	Val Trp Ser Ile Gly Gly Met Ala Val Gly Lys Gly Ile Gln Ser Ser				
134	235	240	245		
136	GGG AAG GTG ATG TAT TTC AGC TCC CTC CCC TAC GTG GTG CTG GCC	1060			

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137	Gly	Val	Met	Tyr	Phe	Ser	Ser	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ala	265
138	250				255				260							265
140	TGC	TTC	CTG	GTC	CGG	GGG	TTG	TTG	CGA	GGG	GCA	GTT	GAT	GGC	ATC	1108
141	Cys	Phe	Leu	Val	Arg	Gly	Leu	Leu	Leu	Arg	Gly	Ala	Val	Asp	Gly	Ile
142					270				275						280	
144	CTA	CAC	ATG	TTC	ACT	CCC	AAG	CTG	GTC	AAG	ATG	CTG	GAC	CCC	CAG	GTG
145	Leu	His	Met	Phe	Thr	Pro	Lys	Leu	Val	Lys	Met	Leu	Asp	Pro	Gln	Val
146					285				290					295		
148	TGG	CGG	GAG	GTA	GCT	ACC	CAG	GTC	TTC	TTT	GGC	TTG	GGT	CTG	GGC	TTT
149	Trp	Arg	Glu	Val	Ala	Thr	Gln	Val	Phe	Phe	Gly	Leu	Gly	Leu	Gly	Phe
150					300				305					310		
152	GGT	GGT	GTC	ATT	GTC	TTC	AGT	TAC	AAT	AAG	CAG	GAC	AAC	AAC	TGC	1204
153	Gly	Gly	Val	Ile	Val	Phe	Ser	Ser	Tyr	Asn	Lys	Gln	Asp	Asn	Asn	Cys
154					315				320				325			
156	CAC	TTC	GAT	GGC	GCC	CTG	GTG	TCC	TTC	ATC	AAC	TTC	TTC	ACG	TCA	GTG
157	His	Phe	Asp	Gly	Ala	Leu	Val	Ser	Phe	Ile	Asn	Phe	Phe	Thr	Ser	Val
158					330				335				340		345	
160	TTG	GCC	ACC	CTC	GTG	GTG	TTT	GTT	GTT	TTG	GGC	TTC	AAG	GCC	AAC	ATC
161	Leu	Ala	Thr	Leu	Val	Val	Phe	Val	Val	Leu	Gly	Phe	Lys	Ala	Asn	Ile
162					350				355				360			
164	ATG	AAT	GAG	AAG	TGT	GTG	GTC	GAG	AAT	GCT	GAG	AAA	ATC	CTA	GGG	TAC
165	Met	Asn	Glu	Lys	Cys	Val	Val	Glu	Asn	Ala	Glu	Lys	Ile	Leu	Gly	Tyr
166					365				370				375			
168	CTT	AAC	ACC	AAC	GTC	CTG	AGC	CGG	GAC	CTC	ATC	CCA	CCC	CAC	GTC	AAC
169	Leu	Asn	Thr	Asn	Val	Leu	Ser	Arg	Asp	Leu	Ile	Pro	Pro	His	Val	Asn
170					380				385				390			
172	TTC	TCC	CAC	CTG	ACC	ACA	AAG	GAC	TAC	ATG	GAG	ATG	GAC	AAT	GTC	ATC
173	Phe	Ser	His	Leu	Thr	Thr	Lys	Asp	Tyr	Met	Glu	Met	Asp	Asn	Val	Ile
174					395				400				405			
176	ATG	ACC	GTG	AAG	GAG	GAC	CAG	TTC	TCA	GCC	CTG	GGC	CTT	GAC	CCC	TGC
177	Met	Thr	Val	Lys	Glu	Asp	Gln	Phe	Ser	Ala	Leu	Gly	Leu	Asp	Pro	Cys
178					410				415				420		425	
180	CTT	CTG	GAG	GAC	CTG	GAC	AAG	TCC	GTG	CAG	GGC	ACA	GGC	CTG	GCC	1588
181	Leu	Leu	Glu	Asp	Glu	Leu	Asp	Lys	Ser	Val	Gln	Gly	Thr	Gly	Leu	Ala
182					430				435				440			
184	TTC	ATC	GCC	TTC	ACT	GAG	GCC	ATG	ACG	CAC	TTC	CCC	ACC	TCC	CCG	TTC
185	Phe	Ile	Ala	Phe	Thr	Glu	Ala	Met	Thr	His	Phe	Pro	Thr	Ser	Pro	Phe
186					445				450				455			
188	TGG	TCC	GTC	ATG	TTC	TTC	TTG	ATG	CTT	ATC	AAC	CTG	GGC	CTG	GGC	AGC
189	Trp	Ser	Val	Met	Phe	Phe	Leu	Met	Leu	Ile	Asn	Leu	Gly	Leu	Gly	Ser
190					460				465				470			
192	ATG	ATC	GGG	ACC	ATG	GCA	GGC	ATC	ACC	ACG	CCC	ATC	ATC	GAC	ACC	TCC
193	Met	Ile	Gly	Thr	Met	Ala	Gly	Ile	Thr	Thr	Pro	Ile	Ile	Asp	Thr	Ser
194					475				480				485			
196	AAG	GTG	CCC	AAG	GAG	ATG	TTC	ACA	GTG	GGC	TGC	TGT	GTC	TTT	ACA	TTC
197	Lys	Val	Pro	Lys	Glu	Met	Phe	Thr	Val	Gly	Cys	Cys	Val	Phe	Thr	Phe
198					490				495				500		505	
200	CTC	GTG	GGA	CTG	TTG	TTC	GTC	CAG	CGC	TCC	GGA	AAC	TAC	TTT	GTC	ACC
201	Leu	Val	Gly	Leu	Leu	Phe	Val	Gln	Arg	Ser	Gly	Asn	Tyr	Phe	Val	Thr

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202	510	515	520	
204	ATG TTC GAT GAC TAC TCA GCC ACG CTG CCA CTC ACT CTC ATC GTC ATC			1876
205	Met Phe Asp Asp Tyr Ser Ala Thr Leu Pro Leu Thr Leu Ile Val Ile			
206	525	530	535	
208	CTT GAG AAC ATC GCT GTG GCC TGG ATT TAT GGA CCC AAG AAG TTC ATG			1924
209	Leu Glu Asn Ile Ala Val Ala Trp Ile Tyr Gly Pro Lys Lys Phe Met			
210	540	545	550	
212	CAG GAG CTG ACG GAG ATG CTG GGC TTC CGC CCC TAC CGC TTC TAT TTC			1972
213	Gln Glu Leu Thr Glu Met Leu Gly Phe Arg Pro Tyr Arg Phe Tyr Phe			
214	555	560	565	
216	TAC ATG TGG AAG TTC GTG TCT CCA CTA TGC ATG GCT GTG CTC ACC ACA			2020
217	Tyr Met Trp Lys Phe Val Ser Pro Leu Cys Met Ala Val Leu Thr Thr			
218	570	575	580	585
220	GCC AGC ATC ATC CAG CTG GGG GTC ACG CCC CCG GCC TAC AGC GCC TGG			2068
221	Ala Ser Ile Ile Gln Leu Gly Val Thr Pro Pro Ala Tyr Ser Ala Trp			
222	590	595	600	
224	ATC AAG GAG GAG GCT GCC GAG CGC TAC CTG TAT TTC CCC AAC TGG CCC			2116
225	Ile Lys Glu Glu Ala Ala Glu Arg Tyr Leu Tyr Phe Pro Asn Trp Pro			
226	605	610	615	
228	ATG GCA CTC CTG ATC ACC CTC ATC GTC GTG GCG ACG CTG CCC ATC CCT			2164
229	Met Ala Leu Leu Ile Thr Leu Ile Val Val Ala Thr Leu Pro Ile Pro			
230	620	625	630	
232	GTC GTG TTC GTC CTG CGG CAC TTC CAC CTG CTC TCT GAT GGC TCC AAC			2212
233	Val Val Phe Val Leu Arg His Phe His Leu Leu Ser Asp Gly Ser Asn			
234	635	640	645	
236	ACC CTC TCC GTG TCC TAC AAG AAG GCC CGC ATG ATG AAG GAC ATC TCC			2260
237	Thr Leu Ser Val Ser Tyr Lys Lys Ala Arg Met Met Lys Asp Ile Ser			
238	650	655	660	665
240	AAC CTG GAG AAC GAT GAG ACC CGC TTC ATC CTC AGC AAG GTG CCC			2308
241	Asn Leu Glu Glu Asn Asp Glu Thr Arg Phe Ile Leu Ser Lys Val Pro			
242	670	675	680	
244	AGT GAG GCA CCT TCC CCC ATG CCC ACT CAC CGT TCC TAT CTG GGG CCC			2356
245	Ser Glu Ala Pro Ser Pro Met Pro Thr His Arg Ser Tyr Leu Gly Pro			
246	685	690	695	
248	GGC AGC ACA TCA CCC CTG GAG ACC AGC TGG AAC CCC AAT GGA CCC TAT			2404
249	Gly Ser Thr Ser Pro Leu Glu Thr Ser Trp Asn Pro Asn Gly Pro Tyr			
250	700	705	710	
252	GGG CGC GGC TAC CTG CTG GCC AGC ACC CCT GAG TCT GAG CTG			2446
253	Gly Arg Gly Tyr Leu Leu Ala Ser Thr Pro Glu Ser Glu Leu			
254	715	720	725	
256	TGACCACTGC CCAAGCCCAT GCCCGCTCTC CCCCCACCG			2485
259	(2) INFORMATION FOR SEQ ID NO: 2:			
261	(i) SEQUENCE CHARACTERISTICS:			
262	(A) LENGTH: 727 amino acids			
263	(B) TYPE: amino acid			
264	(D) TOPOLOGY: linear			
266	(ii) MOLECULE TYPE: protein			
268	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
270	Met Pro Lys Asn Ser Lys Val Thr Gln Arg Glu His Ser Ser Glu His			

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271	1	5	10	15												
273	Val	Thr	Glu	Ser	Val	Ala	Asp	Leu	Leu	Ala	Leu	Glu	Glu	Pro	Val	Asp
274																
		20						25							30	
276	Tyr	Lys	Gln	Ser	Val	Leu	Asn	Val	Ala	Gly	Glu	Ala	Gly	Gly	Lys	Gln
277																
		35						40							45	
279	Lys	Ala	Val	Glu	Glu	Glu	Leu	Asp	Ala	Glu	Asp	Arg	Pro	Ala	Trp	Asn
280								50				60				
								55								
282	Ser	Lys	Leu	Gln	Tyr	Ile	Leu	Ala	Gln	Ile	Gly	Phe	Ser	Val	Gly	Leu
283											70				80	
		65									75					
285	Gly	Asn	Ile	Trp	Arg	Phe	Pro	Tyr	Leu	Cys	Gln	Lys	Asn	Gly	Gly	Gly
286											85				95	
											90					
288	Ala	Tyr	Leu	Val	Pro	Tyr	Leu	Val	Leu	Ile	Ile	Ile	Gly	Ile	Pro	
289								100				105			110	
291	Leu	Phe	Leu	Glu	Leu	Ala	Val	Gly	Gln	Arg	Ile	Arg	Arg	Gly	Ser	
292								115			120			125		
294	Ile	Gly	Val	Trp	His	Tyr	Ile	Cys	Pro	Arg	Leu	Gly	Gly	Ile	Gly	Phe
295								130			135			140		
297	Ser	Ser	Cys	Ile	Val	Cys	Leu	Phe	Val	Gly	Leu	Tyr	Tyr	Asn	Val	Ile
298								145			150			155		160
300	Ile	Gly	Trp	Ser	Ile	Phe	Tyr	Phe	Phe	Lys	Ser	Phe	Gln	Tyr	Pro	Leu
301								165			170			175		
303	Pro	Trp	Ser	Glu	Cys	Pro	Val	Val	Arg	Asn	Gly	Ser	Val	Ala	Val	Val
304								180			185			190		
306	Glu	Ala	Glu	Cys	Glu	Lys	Ser	Ser	Ala	Thr	Thr	Tyr	Phe	Trp	Tyr	Arg
307								195			200			205		
309	Glu	Ala	Leu	Asp	Ile	Ser	Asp	Ser	Ile	Ser	Glu	Ser	Gly	Gly	Leu	Asn
310								210			215			220		
312	Trp	Lys	Met	Thr	Leu	Cys	Leu	Leu	Val	Val	Trp	Ser	Ile	Gly	Gly	Met
313								225			230			235		240
315	Ala	Val	Gly	Lys	Gly	Ile	Gln	Ser	Ser	Gly	Lys	Val	Met	Tyr	Phe	Ser
316								245			250			255		
318	Ser	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ala	Cys	Phe	Leu	Val	Arg	Gly	Leu
319								260			265			270		
321	Leu	Leu	Arg	Gly	Ala	Val	Asp	Gly	Ile	Leu	His	Met	Phe	Thr	Pro	Lys
322								275			280			285		
324	Leu	Val	Lys	Met	Leu	Asp	Pro	Gln	Val	Trp	Arg	Glu	Val	Ala	Thr	Gln
325								290			295			300		
327	Val	Phe	Phe	Gly	Leu	Gly	Leu	Gly	Phe	Gly	Gly	Val	Ile	Val	Phe	Ser
328								305			310			315		320
330	Ser	Tyr	Asn	Lys	Gln	Asp	Asn	Asn	Cys	His	Phe	Asp	Gly	Ala	Leu	Val
331								325			330			335		
333	Ser	Phe	Ile	Asn	Phe	Phe	Thr	Ser	Val	Leu	Ala	Thr	Leu	Val	Val	Phe
334								340			345			350		
336	Val	Val	Leu	Gly	Phe	Lys	Ala	Asn	Ile	Met	Asn	Glu	Lys	Cys	Val	Val
337								355			360			365		
339	Glu	Asn	Ala	Glu	Lys	Ile	Leu	Gly	Tyr	Leu	Asn	Thr	Asn	Val	Leu	Ser
340								370			375			380		
342	Arg	Asp	Leu	Ile	Pro	Pro	His	Val	Asn	Phe	Ser	His	Leu	Thr	Thr	Lys
343								385			390			395		400

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]